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APPLICATION NO.	FILING DATE	FIRST NAMED INVENTOR	ATTORNEY DOCKET NO.	CONFIRMATION NO.
10/063,710	05/08/2002	Audrey Goddard	P3230R1C001-168	8520

30313 7590 01/12/2006

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EXAMINER	
KAUFMAN, CLAIRE M	

ART UNIT	PAPER NUMBER
1646	

DATE MAILED: 01/12/2006

Please find below and/or attached an Office communication concerning this application or proceeding.

Office Action Summary	Application No.	Applicant(s)	
	10/063,710	GODDARD ET AL.	
	Examiner	Art Unit	
	Claire M. Kaufman	1646	

-- The MAILING DATE of this communication appears on the cover sheet with the correspondence address --

Period for Reply

A SHORTENED STATUTORY PERIOD FOR REPLY IS SET TO EXPIRE 3 MONTH(S) OR THIRTY (30) DAYS, WHICHEVER IS LONGER, FROM THE MAILING DATE OF THIS COMMUNICATION.

- Extensions of time may be available under the provisions of 37 CFR 1.136(a). In no event, however, may a reply be timely filed after SIX (6) MONTHS from the mailing date of this communication.
- If NO period for reply is specified above, the maximum statutory period will apply and will expire SIX (6) MONTHS from the mailing date of this communication.
- Failure to reply within the set or extended period for reply will, by statute, cause the application to become ABANDONED (35 U.S.C. § 133). Any reply received by the Office later than three months after the mailing date of this communication, even if timely filed, may reduce any earned patent term adjustment. See 37 CFR 1.704(b).

Status

1)☒ Responsive to communication(s) filed on *31 October 2005*.

2a)☒ This action is **FINAL**. 2b)☐ This action is non-final.

3)☐ Since this application is in condition for allowance except for formal matters, prosecution as to the merits is closed in accordance with the practice under *Ex parte Quayle*, 1935 C.D. 11, 453 O.G. 213.

Disposition of Claims

4)☒ Claim(s) *4-6,11-13,17-20 and 26-32* is/are pending in the application.

4a) Of the above claim(s) _____ is/are withdrawn from consideration.

5)☐ Claim(s) _____ is/are allowed.

6)☒ Claim(s) *4-6,11-13,17-20 and 26-32* is/are rejected.

7)☐ Claim(s) _____ is/are objected to.

8)☐ Claim(s) _____ are subject to restriction and/or election requirement.

Application Papers

9)☐ The specification is objected to by the Examiner.

10)☐ The drawing(s) filed on _____ is/are: a)☐ accepted or b)☐ objected to by the Examiner.

Applicant may not request that any objection to the drawing(s) be held in abeyance. See 37 CFR 1.85(a).

Replacement drawing sheet(s) including the correction is required if the drawing(s) is objected to. See 37 CFR 1.121(d).

11)☐ The oath or declaration is objected to by the Examiner. Note the attached Office Action or form PTO-152.

Priority under 35 U.S.C. § 119

12)☐ Acknowledgment is made of a claim for foreign priority under 35 U.S.C. § 119(a)-(d) or (f).

a)☐ All b)☐ Some * c)☐ None of:

1.☐ Certified copies of the priority documents have been received.

2.☐ Certified copies of the priority documents have been received in Application No. _____.

3.☐ Copies of the certified copies of the priority documents have been received in this National Stage application from the International Bureau (PCT Rule 17.2(a)).

* See the attached detailed Office action for a list of the certified copies not received.

Attachment(s)

1) ☒ Notice of References Cited (PTO-892)
2) ☐ Notice of Draftsperson's Patent Drawing Review (PTO-948)
3) ☒ Information Disclosure Statement(s) (PTO-1449 or PTO/SB/08) Paper No(s)/Mail Date *7/11/05,10/31/05*.
4) ☐ Interview Summary (PTO-413) Paper No(s)/Mail Date. _____.
5) ☐ Notice of Informal Patent Application (PTO-152)
6) ☐ Other: _____.

DETAILED ACTION

Response to Arguments

In response to Applicants' query concerning the status of the rejection of claims 1-6 and 17-20 under 35 USC 103 as unpatentable over GenBank AF184971 made in the Office action mailed 2/8/05, this rejection should have been indicated as withdrawn for the reasons that the rejection of claims under 35 USC 102 as unpatentable over GenBank AF184971 was withdrawn (see page 2 of Office action mailed 7/28/05).

The Examiner incorrectly indicated which claims were rejected under 35 USC 101 for lacking utility. The only claims that should have been indicated as rejected under that statute in the Office action mailed 7/28/05 are claims 14, 16 and 26-31. The rejection of claims 17-20, which depend from claim 4, was in error.

The rejection of claims 14, 16 and 21-25 are moot in view of the cancellation of the claims.

The rejection of claims 17-20 and 26-31 under 35 USC 112, first paragraph, written description, is withdrawn because claims 17-20 were erroneously rejected and Applicants' arguments are persuasive as they pertain to claims 26-31.

The rejection of claims 12 and 13 under 35 USC 102(e) is withdrawn in view of Applicants' arguments.

The text of those sections of Title 35, U.S. Code not included in this action can be found in a prior Office action.

Claim Rejections - 35 USC § 101

Claims 26-31 remain rejected under 35 U.S.C. 101 because the claimed invention lacks patentable utility for the reasons set forth in the previous Office action.

Applicants' arguments pertaining to "immediate benefit", *In re Brana* and *Fujikawa* (pages 6-8 and 14 of the response) were addressed on pages 4 through 6 of the previous Office action.

Applicants argue (*e.g.*, bottom of p. 9) that the asserted utility for the claimed nucleic acid as a diagnostic tool for cancer, particularly esophageal cancer, relies on evidence that the mRNA for the PRO1315 polypeptide is more highly expressed in esophageal cancer. The argument has been fully considered, but is not persuasive. The claims are ***not*** drawn to either 1) the nucleic acid of SEQ ID NO:75, but instead to a nucleic acid at least 95% identical to the coding region of SEQ ID NO:75, or 2) a nucleic acid which must be more highly expressed in esophageal tumor tissue compared to normal esophageal tissue. There is significant structural breadth in the claims and no functional limitation (see below for arguments addressing hybridization as a function). The utility of the nucleic acid of SEQ ID NO:75 (or the coding region thereof) as an esophageal tumor diagnostic does not extend utility to non-identical nucleic acids that may not be more highly expressed in esophageal tumor compared to normal esophageal tissue. As stated in the previous Office action, "Because as previously discussed there is critical information lacking which includes: whether differences in expression between tumor and normal tissue of SEQ ID NO:75 were significant, over what conditions differences could be detected, and what levels (relative or absolute) were detected in tumor and normal control, the skilled artisan cannot use (whether *in vivo* or *in vitro*) the claimed invention if it is not more highly expressed in esophageal tumor than normal esophageal tissue."

Applicants argue (pages 10-11, 14 and 16) that a nucleic acid which hybridizes to a second nucleic acid that is differentially expressed in esophageal tumor and normal tissue is useful as a cancer diagnostic tool. The argument has been fully considered, but is not persuasive. That one skilled in the art would not routinely use a nucleic acid as a tumor probe which is less than 100% identical to a target nucleic acid is a negative teaching, but can be supported by many examples—two of which are provided here. Adams et al. (Science 252 :1651-1656, 1991) describe the expression sequence tags produced for the EST and human genome project. Random-primed and partial cDNA clones were used as probes (p. 1652, second paragraph). While these probes did detect human genes 97% identical to the EST, the probes themselves were the ESTs themselves, not EST that had been altered to be less 100% identical to the original EST sequence (*e.g.* p. 1654, first paragraph). Altering a sequence to make a probe makes the probe less similar to the original sequence to which it is meant to hybridize and makes it that much more similar to a different sequence(s) to which it was not intended to hybridize. WO

97/38085, submitted by Applicants 10/31/05, is directed to identification of genes amplified in cancer cells. Different methods of examining overexpression are discussed. One way is by subtractive hybridization, looking for cDNA which is not completely hybridized (p. 3, lines 27-32). A major drawback of this method is that "it is sensitive to individual phenotypic differences due not just to the presence of cancer, but also through natural metabolic variations." Differential display as well as its drawbacks is discussed from page 3, line 34, to page 4, line 20. Again, false positives caused by detected phenotypic differences are noted. Pertinent to the instant application is that existence of phenotypic differences, allelic variants or splice variants of PRO1315 has apparently not been investigated and remains unknown. On pages 4-6 of WO 97/38085, the method of using a polynucleotide corresponding to cancer-associated genes or fragment of the polynucleotide is discussed. There is no mention of an optimal, routine or preferred method in which the probe has a sequence that has been altered relative to the polynucleotide corresponding to a cancer-associated gene. Because of the risk of false positives and because of the standard of the art, it is maintained that the instant application has neither utility nor is enabled for the hybridizing nucleic acids of claims 26 and 27. Additionally, while the skill in the art for differential screening has existed for over a decade, interpretation of the results depends, for example, on relative or absolute levels of the difference(s), the ability to generalize to more than one cell culture or tumor type or, conversely, the ability to pinpoint a particular tumor type (*e.g.*, adenocarcinoma *versus* squamal), and repeatability of the differential expression both in terms of frequency/prevalence and quantity/sensitivity, none of which information the instant specification provides. Additionally, the utility of a hybridizing probe is not specific because there is no limitation or indication in the specification that the claimed nucleic acid hybridizes selectively/exclusively to SEQ ID NO:75, so as to exclude cross-reactivity with other polynucleotides.

Applicants argue (p. 13) that like the mere identification of a pharmacological activity, identification of an altered expression provides immediate benefit to the pubic. The argument has been fully considered, but is not persuasive. The correct MPEP cite is 2107.01. This citation relates to the Court's decision in *Nelson v. Bowler.* In that decision, the CCPA says that specific therapeutic use of a compound is not necessary if there are tests which evidence pharmacological activity of a compound. In this instance, pharmacological activity is not the same as altered gene

expression. In *Nelson,* the court held that the compound of which utility was in question was shown to have a specific pharmacological activity measured by dispositive tests. "In other words, one skilled in the art at the time the tests were performed would have been reasonably certain that 16-phenoxy PG's had practical utility." (p. 885). "Here, however, a correlation between test results and pharmacological activities has been established." (p. 886) Unlike in *Nelson,* the instant application does not have a showing of practical utility because the specification does not allow the skilled artisan to use the instant invention for the reasons previously discussed. It is maintained that the instant application has not established a correlation between findings of overexpression of nucleic acids **not** identical to the nucleic acid of SEQ ID NO:75 and utility as a cancer diagnostic.

Applicants argue on page 16 that an invention only needs to be partially successful in achieving a useful result for utility (MPEP 2107.01). The argument has been fully considered, but is not persuasive. This passage from the MPEP refers to the issue of an "incredible" utility. That issue has not been raised by the examiner.

Claim Rejections - 35 USC § 112, First Paragraph: Enablement

Claims 4-6, 11-13, 17-20, 26-31 remain and new claim 32 is rejected over 35 U.S.C. 112, first paragraph, as failing to comply with the enablement requirement. The claim(s) contains subject matter which was not described in the specification in such a way as to enable one skilled in the art to which it pertains, or with which it is most nearly connected, to make and/or use the invention for the reasons set forth in the previous Office action and for the following reason addressing new claim 32: The new claim has the same functional limitation as previously rejected claims 4 and 5 and has an intermediate structural limitation between the two claims. It is rejected for the same reasons claims 4 and 5 remain rejected.

Applicants argue on page 18, first paragraph, that "it is unquestionable that one skilled in the art knew how to use a nucleic acid such as the recited nucleic acids in nucleic acid methods such as hybridization assays of samples." The argument has been fully considered, but is not persuasive. It has long been known how to hybridize, however, the issue is that of being able to use the claimed nucleic acid. Using it as generic hybridization probe without a reasonable

expectation it will selectively hybridize to, for example, SEQ ID NO:75 so as to be useful diagnostically makes it not enabled. Even if it did selectively hybridize, because as stated in the previous Office action, there is significant direction and guidance missing in the specification so that the broadly clamed genus of nucleic acids do not have an enabled use. Information lacking includes under what conditions differences can be detected, what levels (relative or absolute) were detected in tumor and normal control, necessary sample size, expression level range for normal and tumor tissues, types of esophageal tissue that can used, and other questions. For these reasons, it is maintained that the specification has not provided the invention in an enabling form.

Applicants argue on page 18 that there is no support of the Examiner's statement that it was not routine to use a probe less than 100% identical to a target sequence and that changing a sequence from 100% to 95% or 99% would not require undue experimentation." The argument has been fully considered, but is not persuasive. First, while it is acknowledged that one could make a sequence less than 100% identical, it is maintained that use of such a sequence is not supported by an enabling disclosure. Neither the specification or claims provide an indication that a hybridizing probe not identical to SEQ ID NO:75 would reasonably be expected to function as a probe to hybridize reasonably exclusively to SEQ ID NO:75, so as to exclude cross-reactivity with other polynucleotides, and that such a probe would have an enabled use as a cancer diagnostic, for which use SEQ ID NO:75 does not have enablement. Some issues of enabling use for a hybridizing probe are very similar to the issue of utility as a probe as discussed above. That one skilled in the art would not routinely use a nucleic acid as a tumor probe which is less than 100% identical to a target nucleic acid is a negative teaching, but can be supported by many examples—two of which are provided here. Adams et al. (Science 252 :1651-1656, 1991) describe the expression sequence tags produced for the EST and human genome project. Random-primed and partial cDNA clones were used as probes (p. 1652, second paragraph). While these probes did detect human genes 97% identical to the EST, the probes themselves were the ESTs themselves, not EST that had been altered to be less 100% identical to the original EST sequence (*e.g.* p. 1654, first paragraph). Altering a sequence to make a probe makes the probe less similar to the original sequence to which it is meant to hybridize and makes it that much more similar to a different sequence(s) to which it was not intended to hybridize. WO

97/38085, submitted by Applicants 10/31/05, is directed to identification of genes amplified in cancer cells. Different methods of examining overexpression are discussed. One way is by subtractive hybridization, looking for cDNA which is not completely hybridized (p. 3, lines 27-32). A major drawback of this method is that "it is sensitive to individual phenotypic differences due not just to the presence of cancer, but also through natural metabolic variations." Differential display as well as its drawbacks is discussed from page 3, line 34, to page 4, line 20. Again, false positives caused by detected phenotypic differences are noted. Pertinent to the instant application is that existence of phenotypic differences, allelic variants or splice variants of PRO1315 has apparently not been investigated and remains unknown. On pages 4-6 of WO 97/38085, the method of using a polynucleotide corresponding to cancer-associated genes or fragment of the polynucleotide is discussed. There is no mention of an optimal, routine or preferred method in which the probe has a sequence that has been altered relative to the polynucleotide corresponding to a cancer-associated gene. Because of the risk of false positives and because of the standard of the art, it is maintained that the instant application has neither utility nor is enabled for the hybridizing nucleic acids of claims 26 and 27. Additionally, while the skill in the art for differential screening has existed for over a decade, interpretation of the results depends, for example, on relative or absolute levels of the difference(s), the ability to generalize to more than one cell culture or tumor type or, conversely, the ability to pinpoint a particular tumor type (*e.g.*, adenocarcinoma *versus* squamal), and repeatability of the differential expression both in terms of frequency/prevalence and quantity/sensitivity, none of which information the instant specification provides.

Applicants argue (bottom of p. 18 and top of p. 20) that Example 18 of the specification shows the results of differential screening that resulted in the finding that the nucleic acid of SEQ ID NO:75 was more highly expressed in esophageal tumor tissue compared to normal esophageal tissue and that the Declaration by Dr. Grimaldi supports the results. The argument has been fully considered, but is not persuasive. These findings apparently used PCR probes identical to portions of SEQ ID NO:75, though **no** probe length or sequence was disclosed. Further, the previously raised issues relating to relative or absolute levels of the difference(s), the ability to generalize to more than one cell culture or tumor type or, conversely, the ability to pinpoint a particular tumor type (*e.g.*, adenocarcinoma *versus* squamal), and repeatability of the

differential expression both in terms of frequency/prevalence and quantity/sensitivity have not been settled. The number and origin of cDNA libraries is not disclosed, except to say that the tumor library was from human esophageal tumor. For these reasons and those previously discussed, Example 18 does not enable the use of the claimed nucleic acids without undue experimentation. As stated in the previous Office action in the paragraph bridging pages 6-7:

> Even though the detection in Example 18 of the specification was carried out using cDNA libraries from tumor and normal tissue sample and, according to the declaration, the libraries were made from pooled samples of tissues, this does not fill the above discussed gaps. It is noted that Grimaldi in paragraph 6 of the declaration describes the detection as "semi-quantitative" and the specification for Example 18 as "standard quantitative". The declaration also says (¶5) that "Data from a pooled sample are more likely to be accurate than data from a single individual." This begs the question of whether the tissue from an individual could be assessed for whether or not it is cancerous. Clinical diagnostics are not usually geared toward a populous but toward an individual's particular condition. While a "relative difference in expression between normal tissue and suspected cancerous tissue" can be informative, without more specifics about necessary sample size, expression level range for normal and tumor tissues, types of esophageal tissue that can used, and other questions, the specification has not provided the invention in an enabling form. Therefore, even accepting Dr. Grimaldi's opinion, the declaration is insufficient to overcome the rejection of the claims under 35 USC 101 and 112, first paragraph, for the reasons discussed above.

Applicants argue (top of p. 19) that if the nucleic acid of claim 4, that is, one that is over expressed in esophageal tumor compared to normal esophageal tumor has utility, then the other claimed nucleic acids have enabled uses. The argument has been fully considered, but is not persuasive. Applicant is reminded that the utility provision of 35 U.S.C. § 101 is distinct from the enablement provision of 35 USC § 112, first paragraph. Also, it is maintained that claims such as 26 do not have utility or enablement. For the reasons discussed above and in the previous Office action, it is maintained that the claims are not enabled.

Applicants argue (bottom of page 19) that the fact that further experimentation is necessary or complex does not make the experimentation undue. The argument has been fully considered, but is not persuasive. Whether experimentation is undue is one factor in determining enablement. For the nucleic acid to be enabled, one skilled in the art must be able to use it based on the description in the specification, prior art and information generally available to one of

skill in the art at the time the application was filed. Applicant is direct to the *Wands* analysis, for example, paragraph bridging pages 4-5 of the previous Office action discussing why it would require undue experimentation to use the claimed invention. It is maintained that the invention is not enabled for the reasons discussed here and in previous Office actions, including the need for undue experimentation.

Applicants argue (bottom of p. 20) that Hu's finding that low expression levels do not necessary correlate with a biologically meaningful role of the gene in cancer does not mean that the gene cannot be used diagnostically for cancer detection. The Examiner agrees with this statement in general. However, even if the role of the gene is not known, the gene must be enabled for diagnostic use, which it is maintained the instantly claimed nucleic acids are not.

Applicants argue in the middle of p. 21 that, "the PTO has apparently accepted that one of skill in the art would know how to make the nucleic acids which are identical to SEQ ID NO:75 and related sequences, as the PTO has not offered any arguments to the contrary." The argument has been fully considered, but is not persuasive. As stated in the previous Office action (mailed 7/28/05) in the last paragraph of p. 8:

> Applicants argue (p. 31) that one skilled in the art would know how to make the claimed nucleic acids. The argument has been fully considered, but is not persuasive. While one could make a nucleic acid which is 95-99% identical to or which hybridizes to SEQ ID NO:75, it would require undue experimentation to make a nucleic which is both 95-99% identical to or which hybridizes to SEQ ID NO:75 and which is more highly expressed in esophageal tumors compared to normal esophageal tissue, respectively. For claims 4 and 5 (and dependent claims 17-20), the nucleic acids need to have not only a particular structural relationship to SEQ ID NO:75, but must also naturally occur in esophageal tumors. The specification has not taught any nucleic acid except SEQ ID NO:75 expressed in those tumors. There is no direction or guidance about predicting what other structurally related nucleic acids would have the necessary expression, nor does the prior art provide information to aid the skilled artisan in this determination.

In the last paragraph of p. 21, Applicants argue that the specification discloses how to find related naturally occurring sequences to SEQ ID NO:75 using probes to screen cancer and normal libraries, and how to determine if the identified nucleic acids are differentially expressed in esophageal tumor compared to matched control tissue. The argument has been fully

considered, but is not persuasive. No sequences for related naturally occurring sequences are disclosed. While one might be able to make and test all possible sequences falling within the structural limitations of the claim, this is an invitation for further significant research. Applicants have not provided guidance for predicting or examples of naturally occurring sequences related to SEQ ID NO:75. The inventors provided only a wish to know.

Applicants argue in the first paragraph of p. 22 that claims 26-31 require only the claimed nucleic acids hybridize and do not require that they be more highly expressed in esophageal tumor compared to normal tissue. The argument has been fully considered, but is not persuasive. While one can make hybridizing nucleic acids, it is maintained for the reasons discussed in previous Office actions and above that one skilled in the art would not know how to use them, particularly as the hybridization conditions do not exclude the possibility or likelihood that the hybridizing nucleic acid would cross-react with a naturally occurring nucleic acid in a tissue, which naturally occurring nucleic acid was not diagnostic for esophageal cancer. The specification does not support a use for a polynucleotide meeting the limitations of claim 26 which is not diagnostic for esophageal cancer.

Claim Rejections - 35 USC § 102

Claims 4, 17, 26 and 28 remain and new claim 32 is rejected under 35 U.S.C. 102(e) as being anticipated by US 5,945,511 for the reasons set forth in the previous Office action and for the following reason addressing new claim 32: New claim 32 is a narrower claim depending from claim 4 which requires 96% instead of 95% identity. Claim 26 was inadvertently and obvious omitted from the previous Office action and should have been included in the rejection since the scope is broader than rejected claim 4 and both claims require 95% identity to SEQ ID NO:75.

Applicants argue that the PTO has not established that the sequence of AF184971 is the same as US 5,945,511. The argument has been fully considered, but is not persuasive. It is noted that the PTO is not required to present alignments to Applicant, but does so in the interest of compact prosecution. Attached to this Office action are four sheets. The first three sheets show the alignment of nucleotide 189-1743 of SEQ ID NO:75 of the instant application to

nucleotide 638 to 2192 of SEQ ID NO:1 of US 5,945,511. The alignment is identical to that with the previous GenBank alignment. The fourth page is an alignment of nucleotides 121-188 of SEQ ID NO:75 of the instant application to nucleotide 569 to 637 of SEQ ID NO:1 of US 5,945,511. In all, SEQ ID NO:1 of US 5,945,511 shares 1276 of the 1329 nucleotide-long coding region of SEQ ID NO:75 of this application to give a shared identity of 96.01%.

Conclusion

THIS ACTION IS MADE FINAL. Applicant is reminded of the extension of time policy as set forth in 37 CFR 1.136(a).

A shortened statutory period for reply to this final action is set to expire THREE MONTHS from the mailing date of this action. In the event a first reply is filed within TWO MONTHS of the mailing date of this final action and the advisory action is not mailed until after the end of the THREE-MONTH shortened statutory period, then the shortened statutory period will expire on the date the advisory action is mailed, and any extension fee pursuant to 37 CFR 1.136(a) will be calculated from the mailing date of the advisory action. In no event, however, will the statutory period for reply expire later than SIX MONTHS from the mailing date of this final action.

Any inquiry concerning this communication or earlier communications from the examiner should be directed to Claire M. Kaufman, whose telephone number is (571) 272-0873. Dr. Kaufman can generally be reached Monday, Tuesday, Thursday and Friday from 9:30AM to 2:30PM.

If attempts to reach the examiner by telephone are unsuccessful, the examiner's supervisor, Brenda Brumback, can be reached at (571) 272-0961.

Any inquiry of a general nature or relating to the status of this application should be directed to the Group receptionist whose telephone number is (571) 272-1600.

Official papers filed by fax should be directed to (571) 273-8300. NOTE: If applicant *does* submit a paper by fax, the original signed copy should be retained by the applicant or applicant's representative. NO DUPLICATE COPIES SHOULD BE SUBMITTED so as to avoid the processing of duplicate papers in the Office.

Information regarding the status of an application may be obtained from the Patent Application Information Retrieval (PAIR) system. Status information for published applications may be obtained from either Private PAIR or Public PAIR. Status information for unpublished applications is available through Private PAIR only. For more information about the PAIR system, see http://pair-direct.uspto.gov. Should you have questions on access to the Private PAIR system, contact the Electronic Business Center (EBC) at 866-217-9197 (toll-free).

Claire M. Kaufman, Ph.D.

Patent Examiner, Art Unit 1646

January 6, 2006

ELIZABETH KEMMERER
PRIMARY EXAMINER

RESULT 1
US-08-943-087-1
; Sequence 1, Application US/08943087
; Patent No. 5945511
; GENERAL INFORMATION:
; APPLICANT: Lok, Si et al.
; TITLE OF INVENTION: CYTOKINE RECEPTOR
; NUMBER OF SEQUENCES: 60
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/943,087
; FILING DATE:
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/803,305
; FILING DATE: 20-FEB-1997
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3516 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: Coding Sequence
; LOCATION: 237...1895
; OTHER INFORMATION:
US-08-943-087-1

121 → 1449 - coding

Query Match 89.1%; Score 1552.4; DB 2; Length 3516;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1553; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Qy        189 ATCACAAATTGGCCCACCAGAGGTGGCACTGACTACAGATGAGAAGTCCATTTCTGTTGT 248
              | ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        638 AACACAAATTGGCCCACCAGAGGTGGCACTGACTACAGATGAGAAGTCCATTTCTGTTGT 697

Qy        249 CCTGACAGCTCCAGAGAAGTGGAAGAGAAATCCAGAAGACCTTCCTGTTTCCATGCAACA 308
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        698 CCTGACAGCTCCAGAGAAGTGGAAGAGAAATCCAGAAGACCTTCCTGTTTCCATGCAACA 757

Qy        309 AATATACTCCAATCTGAAGTATAACGTGTCTGTGTTGAATACTAAATCAAACAGAACGTG 368
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        758 AATATACTCCAATCTGAAGTATAACGTGTCTGTGTTGAATACTAAATCAAACAGAACGTG 817

Qy        369 GTCCCAGTGTGTGACCAACCACACGCTGGTGCTCACCTGGCTGGAGCCGAACACTCTTTA 428
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        818 GTCCCAGTGTGTGACCAACCACACGCTGGTGCTCACCTGGCTGGAGCCGAACACTCTTTA 877

Qy        429 CTGCGTACACGTGGAGTCCTTCGTCCCAGGGCCCCCTCGCCGTGCTCAGCCTTCTGAGAA 488
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        878 CTGCGTACACGTGGAGTCCTTCGTCCCAGGGCCCCCTCGCCGTGCTCAGCCTTCTGAGAA 937

Qy        489 GCAGTGTGCCAGGACTTTGAAAGATCAATCATCAGAGTTCAAGGCTAAAATCATCTTCTG 548
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        938 GCAGTGTGCCAGGACTTTGAAAGATCAATCATCAGAGTTCAAGGCTAAAATCATCTTCTG 997

Qy        549 GTATGTTTTGCCCATATCTATTACCGTGTTTCTTTTTTCTGTGATGGGCTATTCCATCTA 608
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Db        998 GTATGTTTTGCCCATATCTATTACCGTGTTTCTTTTTTCTGTGATGGGCTATTCCATCTA 1057

Qy        609 CCGATATATCCACGTTGGCAAAGAGAAACACCCAGCAAATTTGATTTTGATTTATGGAAA 668

Db       1058 CCGATATATCCACGTTGGCAAAGAGAAACACCCAGCAAATTTGATTTTGATTTATGGAAA 1117

Qy        669 TGAATTTGACAAAAGATTCTTTGTGCCTGCTGAAAAAATCGTGATTAACTTTATCACCCT 728

Db       1118 TGAATTTGACAAAAGATTCTTTGTGCCTGCTGAAAAAATCGTGATTAACTTTATCACCCT 1177

Qy        729 CAATATCTCGGATGATTCTAAAATTTCTCATCAGGATATGAGTTTACTGGGAAAAAGCAG 788

Db       1178 CAATATCTCGGATGATTCTAAAATTTCTCATCAGGATATGAGTTTACTGGGAAAAAGCAG 1237

Qy        789 TGATGTATCCAGCCTTAATGATCCTCAGCCCAGCGGGAACCTGAGGCCCCCTCAGGAGGA 848

Db       1238 TGATGTATCCAGCCTTAATGATCCTCAGCCCAGCGGGAACCTGAGGCCCCCTCAGGAGGA 1297

Qy        849 AGAGGAGGTGAAACATTTAGGGTATGCTTCGCATTTGATGGAAATTTTTTGTGACTCTGA 908

Db       1298 AGAGGAGGTGAAACATTTAGGGTATGCTTCGCATTTGATGGAAATTTTTTGTGACTCTGA 1357

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Qy       1029 TGAAGAGCAGGAGCTCAGTTTGCAGGAGGAGGTGTCCACACAAGGAACATTATTGGAGTC 1088

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Db       1538 GCAGGCAGCGTTGGCAGTCTTGGGCCCGCAAACGTTACAGTACTCATACACCCCTCAGCT 1597

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Db       1658 GCCATCGACGACCCTGGTCGACTGGGATCCCCAAACTGGCAGGCTGTGTATTCCTTCGCT 1717

Qy       1269 GTCCAGCTTCGACCAGGATTCAGAGGGCTGCGAGCCTTCTGAGGGGGATGGGCTCGGAGA 1328

Db       1718 GTCCAGCTTCGACCAGGATTCAGAGGGCTGCGAGCCTTCTGAGGGGGATGGGCTCGGAGA 1777

Qy       1329 GGAGGGTCTTCTATCTAGACTCTATGAGGAGCCGGCTCCAGACAGGCCACCAGGAGAAAA 1388

Db       1778 GGAGGGTCTTCTATCTAGACTCTATGAGGAGCCGGCTCCAGACAGGCCACCAGGAGAAAA 1837

Qy       1389 TGAAACCTATCTCATGCAATTCATGGAGGAATGGGGGTTATATGTGCAGATGGAAAACTG 1448
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STOP
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Qy       1509 CCCAGCCATAAAGTACCTGGGATGAAAGAAGTTTTTTCCAGTTTGTCAGTGTCTGTGAGA 1568
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Qy       1569 ATTACTTATTTCTTTTCTCTATTCTCATAGCACGTGTGTGATTGGTTCATGCATGTAGGT 1628
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Qy       1629 CTCTTAACAATGATGGTGGGCCTCTGGAGTCCAGGGGCTGGCCGGTTGTTCTATGCAGAG 1688
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Qy       1689 AAAGCAGTCAATAAATGTTTGCCAGACTGGGTGCAGAATTTATTCAGGTGGGTGT 1743
              |||||||||||||||||||||||||||||||||||||||||||||||||||||
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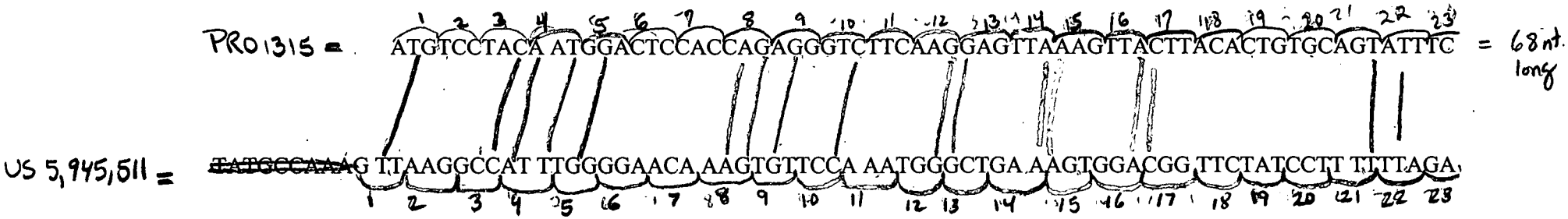

17 matches + 1259

% identity w/coding region of SEQ ID NO:75 = $\frac{1276}{1329}$ = 96.01%

~~aaa acaaattggc ccaccagagg~~